

A NOVEL MAMMALIAN GENE, *bcl-w*, BELONGS TO THE *bcl-2* FAMILY OF APOPTOSIS-CONTROLLING GENES

5 The present invention is broadly directed to therapeutic molecules capable of *inter alia* modulating apoptosis in mammalian cells. The therapeutic molecules of the present invention encompass genetic sequences and chemical entities capable of regulating expression of a novel mammalian gene belonging to the *bcl-2* family and which promotes cell survival. The therapeutic molecules of the present invention may have further utility in delaying cell cycle  
10 entry. In addition, the present invention extends to chemical entities capable of modulating activity and function of the translation product of said novel gene of the *bcl-2* family. The present invention also extends to the translation product of the novel gene of the *bcl-2* family and its use in, for example, therapy, diagnosis, antibody generation and as a screening tool for therapeutic molecules capable of modulating physiological cell death or survival and/or  
15 modulating cell cycle entry.

Bibliographic details of the publications numerically referred to in this specification are collected at the end of the description. Sequence Identity Numbers (SEQ ID NOs.) for the nucleotide and amino acid sequences referred to in the specification are defined following the  
20 Bibliography. A summary of the SEQ ID NOs. is provided before the Examples

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other  
25 element or integer or group of elements or integers.

The increasing sophistication of recombinant DNA technology is greatly facilitating research and development in the medical and allied health fields. This technology is becoming particularly important in research into the treatment and diagnosis of both proliferative cell  
30 disorders such as cancers and sarcomas and in degenerative diseases such as some autoimmune

conditions. There is a need to identify and characterise at the genetic level the elements involved in cell survival and physiological cell death (apoptosis).

Apoptosis is accomplished by a process that is conserved between organisms as diverse as  
5 nematodes and man. Positive and negative regulation of cell survival is essential for the proper development and differentiation of the embryo and for ensuring homeostasis in adult tissues. Cell survival can be promoted by the binding of growth factors to their receptors or by interaction of cellular adhesion molecules. A range of cytotoxic agents can counteract these signals and activate apoptosis, a process initially defined by specific morphologic criteria, such  
10 as chromatin condensation, cell compaction, membrane blebbing and, often, internucleosomal cleavage of DNA.

The biochemical details of the intracellular pathways governing cell survival and death remain largely undefined. However, several key regulators have emerged. The first to be discovered  
15 was Bcl-2, a 26 kD cytoplasmic protein encoded by the *bcl-2* gene translocated to the IGH locus in human follicular lymphoma. High levels of Bcl-2 greatly enhance the ability of cells to survive cytokine deprivation and a wide variety of other cytotoxic conditions, including DNA damage.

20 The mammalian genome contains other genes homologous to *bcl-2* but which differ in function. For example, *bcl-x* blocks apoptosis (Boise *et al*, 1993) whereas *bax* and *bak* inhibit the survival function of *bcl-2* and *bcl-x* (Oltvai *et al*, 1993; Chittenden *et al*, 1995; Farrow *et al*, 1995; Kiefer *et al*, 1995). Due to the potential importance of cell apoptosis controlling genes in the treatment of cancers and sarcomas and in the treatment of degenerative disorders, there is a  
25 need to identify new genes homologous to *bcl-2* in structure and function.

In accordance with the present invention, the inventors have identified a novel gene from mammals designated herein "*bcl-w*". Gene transfer studies show that *bcl-w* enhances cell survival and belongs to the *bcl-2* family of apoptosis-controlling genes. The identification of  
30 this new gene will lead to the generation of a range of therapeutic molecules capable of acting

as either antagonists or agonists of *bcl-w* expression or activity and will be useful in cancer or degenerative disease therapy. The identification of the gene will also permit the production of vast quantities of recombinant translation products for use in therapy, diagnosis, antibody generation and as a screen for therapeutic molecules capable of modulating physiological cell  
5 deaths or survival including modulating cell cycle entry.

Accordingly, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence encoding or complementary to a sequence encoding a novel mammalian gene from the *bcl-2* family and comprising an amino acid sequence substantially as set forth  
10 in SEQ ID NO:7 or SEQ ID NO:9 or having 47% or greater similarity to either of SEQ ID NO:7 or SEQ ID NO:9.

Another aspect of the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence encoding or complementary to a sequence encoding the amino acid  
15 sequence set forth in SEQ ID NO:7 or SEQ ID NO:9 or a derivative thereof or encoding an amino acid sequence having 47% or greater similarity to either SEQ ID NO:7 or SEQ ID NO:9.

The term "similarity" as used herein includes exact identity between compared sequences at the nucleotide or amino acid level. Where there is non-identity at the nucleotide level, "similarity"  
20 includes differences between sequences which result in different amino acids that are nevertheless related to each other at the structural, functional, biochemical and/or conformational levels. Where there is non-identity at the amino acid level, "similarity" includes amino acids that are nevertheless related to each other at the structural, functional, biochemical and/or conformational levels.

25

Preferably, the percentage similarity is between 48% and 100% inclusive such as approximately 50% or 55%, 59% or 65%, 70% or 75%, 80% or 85%, 90% or 95% or greater than 96% or a percentage similarity therebetween.

30 Another aspect of the present invention provides a nucleic acid molecule comprising a sequence

- 4 -

of nucleotides substantially as set forth in SEQ ID NO:6 or SEQ ID NO:8 or a nucleotide sequence encoding an amino acid sequence having 47% or greater similarity to SEQ ID NO:7 or SEQ ID NO:9.

5 The nucleic acid molecule according to this aspect of the present invention corresponds herein to "*bcl-w*". This gene has been determined by the inventors in accordance with the present invention to enhance cell survival. The product of the *bcl-w* gene is referred to as Bcl-w. Human Bcl-w is defined by the amino acid sequence set forth in SEQ ID NO:7 and mouse Bcl-w is defined in SEQ ID NO:9. The respective nucleotide sequences from human *bcl-w* and  
10 mouse *bcl-w* are shown in SEQ ID NO:6 and SEQ ID NO:8 respectively. Reference herein to "*bcl-w*" includes reference to derivatives thereof includes single or multiple nucleotide substitutions, deletions and/or additions. Similarly, reference herein to "Bcl-w" includes all derivatives including amino acid substitutions, deletions and/or additions. The gene is preferably from a human, primate, livestock animal (sheep, pig, cow, horse, donkey), laboratory  
15 test animal (eg. mouse, rat, rabbit, guinea pig), companion animal (eg. dog, cat) or captive wild animal (eg. fox, kangaroo, deer).

Although the present invention relates to a mammalian homologue of Bcl-w having an amino acid sequence of 47% or greater similarity to SEQ ID NO:7 or SEQ ID NO:8, the subject  
20 invention does extend to novel Bcl-w homologues from any animal including a mammal previously undisclosed.

Accordingly, another aspect of the present invention provides a nucleic acid molecule comprising a sequence of nucleotides encoding human Bcl-w or a derivative thereof, said  
25 human Bcl-w having an amino acid sequence substantially as set forth in SEQ ID NO:7 or is a mammalian homologue thereof having an amino acid sequence of substantially 47% or greater similarity to the amino acid sequence set forth in SEQ ID NO:7.

A further aspect provides a nucleic acid molecule comprising a sequence of nucleotides  
30 encoding human Bcl-w or a derivative thereof, said murine Bcl-w having an amino acid

sequence substantially as set forth in SEQ ID NO:9 or is a mammalian homologue thereof having an amino acid sequence of substantially 47% or greater similarity to the amino acid sequence set forth in SEQ ID NO:9.

- 5 The nucleic acid molecule of the present invention is preferably in isolated form or ligated to a vector, such as an expression vector. By "isolated" is meant a nucleic acid molecule having undergone at least one purification step and this is conveniently defined, for example, by a composition comprising at least about 10% subject nucleic acid molecule, preferably at least about 20%, more preferably at least about 30%, still more preferably at least about 40-50%,  
10 even still more preferably at least about 60-70%, yet even still more preferably 80-90% or greater of subject nucleic acid molecule relative to other components as determined by molecular weight, encoding activity, nucleotide sequence, base composition or other convenient means. The nucleic acid molecule of the present invention may also be considered, in a preferred embodiment, to be biologically pure.

15

- The nucleic acid molecule encoding *bcl-w* is preferably a sequence of deoxyribonucleic acids such as cDNA sequence or a genomic sequence. A genomic sequence may also comprise exons and introns. A genomic sequence may also include a promoter region or other regulatory region. In a particularly preferred embodiment, the nucleotide sequence corresponding to *bcl-w*  
20 is a cDNA sequence comprising a sequence of nucleotides as set forth in SEQ ID NO:6 (human) or SEQ ID NO:8 (mouse) or is a derivative thereof including a nucleotide sequence having similar to SEQ ID NO:6 or SEQ ID NO:8 but which encodes an amino acid sequence having 47% or greater similarity to either SEQ ID NO:7 or SEQ ID NO:9.

- 25 The term "derivative" as used herein includes portions, fragments, parts, homologues or analogues of the nucleic acid molecule or a translation product thereof. A derivative may also be a single or multiple nucleotide or amino acid substitution, deletion and/or addition. A derivative of the nucleic acid molecule of the present invention also includes nucleic acid molecules capable of hybridizing to the nucleotide sequence set forth in SEQ ID NO:6 or SEQ  
30 ID NO:8 under low stringency conditions. Preferably, the low stringency is at 42°C.

More particularly, the present invention provides a nucleic acid molecule comprising a nucleotide sequence substantially as set forth in SEQ ID NO:6 or SEQ ID NO:8 or a derivative or homologue thereof capable of hybridizing to SEQ ID NO:6 or SEQ ID NO:8 under low stringency conditions and which encodes an amino acid sequence having 47% or greater  
5 similarity to the amino acid sequence set forth in SEQ ID NO:7 or SEQ ID NO:9.

Reference herein to a low stringency at 42°C includes and encompasses from at least about 1% v/v to at least about 15% v/v formamide and from at least about 1M to at least about 2M salt for hybridisation, and at least about 1M to at least about 2M salt for washing conditions.  
10 Alternative stringency conditions may be applied where necessary, such as medium stringency, which includes and encompasses from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5M to at least about 0.9M salt for hybridisation, and at least about 0.5M to at least about 0.9M salt for washing conditions, or high stringency, which includes and encompasses from at least about 31% v/v to at least about 50% v/v formamide and  
15 from at least about 0.01M to at least about 0.15M salt for hybridisation, and at least about 0.01M to at least about 0.15M salt for washing conditions.

The derivatives of the nucleic acid molecule of the present invention include oligonucleotides, PCR primers, antisense molecules, molecules suitable for use in co-suppression and fusion  
20 nucleic acid molecules. Some molecules are also contemplated capable of regulating expression of *bcl-w*. The present invention also contemplates ribozymes directed to *bcl-w*. The derivatives of the Bcl-w translation product of the present invention include fragments having particular epitopes or parts of the entire Bcl-w protein fused to peptides, polypeptides or other proteins. Catalytic antibodies are also contemplated to Bcl-w or derivatives thereof. Such  
25 catalytic antibodies would be useful for controlling or otherwise modulating Bcl-w. The catalytic antibodies or other regulatory molecules may need to be modified to facilitate entry into the cells. Alternatively, they may be genetically produce in transgenic cells or introduced via a viral or other suitable vector.

30 In another embodiment the present invention is directed to an isolated nucleic acid molecule

- 7 -

encoding *bcl-w* or a derivative thereof, said nucleic acid molecule selected from the list consisting of:

- 5 (I) a nucleic acid molecule comprising a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:7 or SEQ ID NO:9 or having 47% or greater similarity for SEQ ID NO:7 or SEQ ID NO:9;
- (ii) a nucleic acid molecule comprising a nucleotide sequence substantially as set forth in SEQ ID NO:6 or SEQ ID NO:8 or comprising a nucleotide sequence encoding an amino acid sequence of 47% or greater similarity to SEQ ID NO:7 or SEQ ID NO:9;
- 10 (iii) a nucleic acid molecule capable of hybridizing to the nucleotide sequence substantially set forth in SEQ ID NO:6 or SEQ ID NO:8 under low stringency conditions and encoding an amino acid sequence having of 47% or greater similarity to SEQ ID NO:7 or SEQ ID NO:9;
- (iv) a nucleic acid molecule capable of hybridizing to the nucleic acid of part (I) or (ii) or
- 15 (iii) under low stringency conditions and encoding an amino acid sequence having 47% or greater similarity to SEQ ID NO:7 or SEQ ID NO:9; and
- (v) a derivative or mammalian homologue of the nucleic acid molecule of parts (I) or (ii) or (iii) or (iv).

20 The mammalian homologues contemplated in part (v) of the previous paragraph are novel homologues and do not encompass, for example, known Bcl-2. As stated above, novel homologues of Bcl-w falling outside of the definition herein described are also contemplated by the present invention.

25 The nucleic acid molecule may be ligated to an expression vector capable of expression in a prokaryotic cell (e.g. *E.coli*) or a eukaryotic cell (e.g. yeast cells, fungal cells, insect cells, mammalian cells or plant cells). The nucleic acid molecule may be ligated or fused or otherwise associated with a nucleic acid molecule encoding another entity such as a signal peptide, a cytokine or other member of the Bcl-2 family.



- 8 -

The present invention extends to the expression product of the nucleic acid molecule hereinbefore defined.

The expression product is Bcl-w having an amino acid sequence set forth in SEQ ID NO:7 or  
5 SEQ ID NO:9 or is a derivative thereof as defined above or is a mammalian homologue having an amino acid sequence of 47% or greater similarity to the amino acid sequence set forth in SEQ ID NO:7 or SEQ ID NO:9. A derivative may be a single or multiple amino acid substitution, deletion and/or addition. Other derivatives include chemical analogues of Bcl-w. Analogues of Bcl-w contemplated herein include, but are not limited to, modification to side  
10 chains, incorporating of unnatural amino acids and/or their derivatives during peptide, polypeptide or protein synthesis and the use of crosslinkers and other methods which impose conformational constraints on the proteinaceous molecule or their analogues.

Another aspect of the present invention is directed to an isolated polypeptide selected from the  
15 listing consisting of:

- (i) a polypeptide having an amino acid sequence substantially as set forth in SEQ ID NO:7 or SEQ ID NO:9 or a sequence having 47% or greater similarity to SEQ ID NO:7 or SEQ ID NO:9;
- 20 (ii) a polypeptide encoded by a nucleotide sequence substantially as set forth in SEQ ID NO:6 or SEQ ID NO:8 or a sequence encoding an amino acid sequence having 47% or greater similarity to SEQ ID NO:7 or SEQ ID NO:9;
- (iii) a polypeptide encoded by a nucleic acid molecule capable of hybridizing to the nucleotide sequence set forth in SEQ ID NO:6 or SEQ ID NO:8 under low stringency  
25 conditions and which encodes an amino acid sequence substantially as set forth in SEQ ID NO:7 or SEQ ID NO:9 or an amino acid sequence having 47% or greater similarity to SEQ ID NO:7 or SEQ ID NO:9;
- (iv) a polypeptide as defined in part (i) or (ii) or (iii) in homodimeric form; and
- (v) a polypeptide as defined in part (i) or (ii) or (iii) in heterodimeric form.



A derivative may carry a mutation anywhere in the Bcl-w molecule such as but not limited to the S1 and/or S2 region. For example, a substitution at position 94 in S2 from Gly to Glu is encompassed by the present invention. Other areas of Bcl-w for which mutations are contemplated include but are not limited to the region immediately N-terminal to S2, the NH1  
5 region, the S3 region, the S2-S3 region and the BH3 region.

Examples of side chain modifications contemplated by the present invention include modifications of amino groups such as by reductive alkylation by reaction with an aldehyde followed by reduction with NaBH<sub>4</sub>; amidination with methylacetimidate; acylation with acetic  
10 anhydride; carbamoylation of amino groups with cyanate; trinitrobenzylation of amino groups with 2, 4, 6-trinitrobenzene sulphonic acid (TNBS); acylation of amino groups with succinic anhydride and tetrahydrophthalic anhydride; and pyridoxylation of lysine with pyridoxal-5-phosphate followed by reduction with NaBH<sub>4</sub>.

15 The guanidine group of arginine residues may be modified by the formation of heterocyclic condensation products with reagents such as 2,3-butanedione, phenylglyoxal and glyoxal.

The carboxyl group may be modified by carbodiimide activation *via* O-acylisourea formation followed by subsequent derivitisation, for example, to a corresponding amide.

20

Sulphydryl groups may be modified by methods such as carboxymethylation with iodoacetic acid or iodoacetamide; performic acid oxidation to cysteic acid; formation of a mixed disulphides with other thiol compounds; reaction with maleimide, maleic anhydride or other substituted maleimide; formation of mercurial derivatives using 4-chloromercuribenzoate, 4-  
25 chloromercuriphenylsulphonic acid, phenylmercury chloride, 2-chloromercuri-4-nitrophenol and other mercurials; carbamoylation with cyanate at alkaline pH.

Tryptophan residues may be modified by, for example, oxidation with N-bromosuccinimide or alkylation of the indole ring with 2-hydroxy-5-nitrobenzyl bromide or sulphenyl halides.

30 Tyrosine residues on the other hand, may be altered by nitration with tetranitromethane to form

a 3-nitrotyrosine derivative.

Modification of the imidazole ring of a histidine residue may be accomplished by alkylation with iodoacetic acid derivatives or N-carbethoxylation with diethylpyrocarbonate.

5

Examples of incorporating unnatural amino acids and derivatives during peptide synthesis include, but are not limited to, use of norleucine, 4-amino butyric acid, 4-amino-3-hydroxy-5-phenylpentanoic acid, 6-aminohexanoic acid, t-butylglycine, norvaline, phenylglycine, ornithine, sarcosine, 4-amino-3-hydroxy-6-methylheptanoic acid, 2-thienyl alanine and/or D-  
10 isomers of amino acids. A list of unnatural amino acid, contemplated herein is shown in Table 1.

Crosslinkers can be used, for example, to stabilise 3D conformations, using homo-bifunctional crosslinkers such as the bifunctional imido esters having  $(CH_2)_n$  spacer groups with  $n=1$  to  
15  $n=6$ , glutaraldehyde, N-hydroxysuccinimide esters and hetero-bifunctional reagents which usually contain an amino-reactive moiety such as N-hydroxysuccinimide and another group specific-reactive moiety such as maleimido or dithio moiety (SH) or carbodiimide (COOH). In addition, peptides can be conformationally constrained by, for example, incorporation of  $C_\alpha$  and  $N_\alpha$ -methylamino acids, introduction of double bonds between  $C_\alpha$  and  $C_\beta$  atoms of amino  
20 acids and the formation of cyclic peptides or analogues by introducing covalent bonds such as forming an amide bond between the N and C termini, between two side chains or between a side chain and the N or C terminus.

The identification of *bcl-w* permits the generation of a range of therapeutic molecules capable  
25 of modulating expression of *bcl-w* or modulating the activity of Bcl-2. Modulators contemplated by the present invention includes agonists and antagonists of *bcl-w* expression. Antagonists of *bcl-w* expression include antisense molecules, ribozymes and co-suppression molecules. Agonists include molecules which increase promoter ability or interfere with negative regulatory mechanisms. Agonists of Bcl-w include molecules which overcome any  
30 negative regulatory mechanism. Antagonists of Bcl-w include antibodies and inhibitor peptide

**WO 97/35971**

**PCT/AU97/00199**

- 11 -

fragments.

[illegible]

TABLE 1

Non-conventional amino acid	Code	Non-conventional amino acid	Code
5 $\alpha$ -aminobutyric acid	Abu	L-N-methylalanine	Nmala
$\alpha$ -amino- $\alpha$ -methylbutyrate	Mgab	L-N-methylarginine	Nmarg
aminocyclopropane-	Cpro	L-N-methylasparagine	Nmasn
carboxylate		L-N-methylaspartic acid	Nmasp
10 aminoisobutyric acid	Aib	L-N-methylcysteine	Nmcys
aminonorbornyl-	Norb	L-N-methylglutamine	Nmgln
carboxylate		L-N-methylglutamic acid	Nmglu
cyclohexylalanine		Chexa L-N-methylhistidine	Nmhis
cyclopentylalanine	Cpen	L-N-methylisoleucine	Nmile
15 D-alanine	Dal	L-N-methylleucine	Nmleu
D-arginine	Darg	L-N-methyllysine	Nmlys
D-aspartic acid	Das	L-N-methylmethionine	Nmmet
D-cysteine	Dcys	L-N-methylnorleucine	Nmnle
D-glutamine	Dgln	L-N-methylnorvaline	Nmnva
20 D-glutamic acid	Dglu	L-N-methylornithine	Nmorn
D-histidine	Dhis	L-N-methylphenylalanine	Nmphe
D-isoleucine	Dile	L-N-methylproline	Nmpro
D-leucine	Dleu	L-N-methylserine	Nmser
D-lysine	Dlys	L-N-methylthreonine	Nmthr
25 D-methionine	Dmet	L-N-methyltryptophan	Nmtrp
D-ornithine	Dorn	L-N-methyltyrosine	Nmtyr
D-phenylalanine	Dphe	L-N-methylvaline	Nmval
D-proline	Dpro	L-N-methylethylglycine	Nmetg
D-serine	Dser	L-N-methyl-t-butylglycine	Nmtbug
30 D-threonine	Dthr	L-norleucine	Nle

	D-tryptophan	Dtrp	L-norvaline	Nva
	D-tyrosine	Dtyr	$\alpha$ -methyl-aminoisobutyrate	Maib
	D-valine	Dval	$\alpha$ -methyl- $\gamma$ -aminobutyrate	Mgabv
	D- $\alpha$ -methylalanine	Dmala	$\alpha$ -methylcyclohexylalanine	Mchexa
5	D- $\alpha$ -methylarginine	Dmarg	$\alpha$ -methylcyclopentylalanine	Mcpen
	D- $\alpha$ -methylasparagine	Dmasn	$\alpha$ -methyl- $\alpha$ -naphthylalanine	Manap
	D- $\alpha$ -methylaspartate	Dmasp	$\alpha$ -methylpenicillamine	Mpen
	D- $\alpha$ -methylcysteine	Dmcys	N-(4-aminobutyl)glycine	Nglu
	D- $\alpha$ -methylglutamine	Dmgln	N-(2-aminoethyl)glycine	Naeg
10	D- $\alpha$ -methylhistidine	Dmhis	N-(3-aminopropyl)glycine	Norn
	D- $\alpha$ -methylisoleucine	Dmile	N-amino- $\alpha$ -methylbutyrate	Nmaabu
	D- $\alpha$ -methylleucine	Dmleu	$\alpha$ -naphthylalanine	Anap
	D- $\alpha$ -methyllysine	Dmlys	N-benzylglycine	Nphe
	D- $\alpha$ -methylmethionine	Dmmet	N-(2-carbamylethyl)glycine	Ngln
15	D- $\alpha$ -methylornithine	Dmorn	N-(carbamylmethyl)glycine	Nasn
	D- $\alpha$ -methylphenylalanine	Dmphe	N-(2-carboxyethyl)glycine	Nglu
	D- $\alpha$ -methylproline	Dmpro	N-(carboxymethyl)glycine	Nasp
	D- $\alpha$ -methylserine	Dmser	N-cyclobutylglycine	Ncbut
	D- $\alpha$ -methylthreonine	Dmthr	N-cycloheptylglycine	Nchep
20	D- $\alpha$ -methyltryptophan	Dmtrp	N-cyclohexylglycine	Nchex
	D- $\alpha$ -methyltyrosine	Dmtty	N-cyclodecylglycine	Ncdec
	D- $\alpha$ -methylvaline	Dmval	N-cylcododecylglycine	Ncdod
	D-N-methylalanine	Dnmala	N-cyclooctylglycine	Ncoct
	D-N-methylarginine	Dnmarg	N-cyclopropylglycine	Ncpro
25	D-N-methylasparagine	Dnmasn	N-cycloundecylglycine	Ncund
	D-N-methylaspartate	Dnmasp	N-(2,2-diphenylethyl)glycine	Nbhm
	D-N-methylcysteine	Dnmcys	N-(3,3-diphenylpropyl)glycine	Nbhe
	D-N-methylglutamine	Dnmgln	N-(3-guanidinopropyl)glycine	Narg
	D-N-methylglutamate	Dnmglu	N-(1-hydroxyethyl)glycine	Nthr
30	D-N-methylhistidine	Dnmhis	N-(hydroxyethyl)glycine	Nser

D-N-methylisoleucine	Dnmile	N-(imidazolylethyl)glycine	Nhis
D-N-methylleucine	Dnmleu	N-(3-indolylyethyl)glycine	Nhtrp
D-N-methyllysine	Dnmlys	N-methyl- $\gamma$ -aminobutyrate	Nmgabu
N-methylcyclohexylalanine	Nmchexa	D-N-methylmethionine	Dnmmt
5 D-N-methylornithine	Dnmorn	N-methylcyclopentylalanine	Nmcpn
N-methylglycine	Nala	D-N-methylphenylalanine	Dnmphe
N-methylaminoisobutyrate	Nmaib	D-N-methylproline	Dnmpro
N-(1-methylpropyl)glycine	Nile	D-N-methylserine	Dnmser
N-(2-methylpropyl)glycine	Nleu	D-N-methylthreonine	Dnmthr
10 D-N-methyltryptophan	Dnmtrp	N-(1-methylethyl)glycine	Nval
D-N-methyltyrosine	Dnmtyr	N-methyl- $\alpha$ -naphthylalanine	Nmanap
D-N-methylvaline	Dnmval	N-methylpenicillamine	Nmpen
$\gamma$ -aminobutyric acid	Gabu	N-( <i>p</i> -hydroxyphenyl)glycine	Nhtyr
L- <i>t</i> -butylglycine	Tbug	N-(thiomethyl)glycine	Ncys
15 L-ethylglycine	Etg	penicillamine	Pen
L-homophenylalanine	Hphe	L- $\alpha$ -methylalanine	Mala
L- $\alpha$ -methylarginine	Marg	L- $\alpha$ -methylasparagine	Masn
L- $\alpha$ -methylaspartate	Masp	L- $\alpha$ -methyl- <i>t</i> -butylglycine	Mtbug
L- $\alpha$ -methylcysteine	Mcys	L-methylethylglycine	Metg
20 L- $\alpha$ -methylglutamine	Mgln	L- $\alpha$ -methylglutamate	Mglu
L- $\alpha$ -methylhistidine	Mhis	L- $\alpha$ -methylhomophenylalanine	Mhphe
L- $\alpha$ -methylisoleucine	Mile	N-(2-methylthioethyl)glycine	Nmet
L- $\alpha$ -methylleucine	Mleu	L- $\alpha$ -methyllysine	Mlys
L- $\alpha$ -methylmethionine	Mmet	L- $\alpha$ -methylnorleucine	Mnle
25 L- $\alpha$ -methylnorvaline	Mnva	L- $\alpha$ -methylornithine	Morn
L- $\alpha$ -methylphenylalanine	Mphe	L- $\alpha$ -methylproline	Mpro
L- $\alpha$ -methylserine	Mser	L- $\alpha$ -methylthreonine	Mthr
L- $\alpha$ -methyltryptophan	Mtrp	L- $\alpha$ -methyltyrosine	Mtyr

- 15 -

L- $\alpha$ -methylvaline	Mval	L-N-methylhomophenylalanine	Nmhphe
N-(N-(2,2-diphenylethyl)	Nnbhm	N-(N-(3,3-diphenylpropyl)	Nnbhe
carbamylmethyl)glycine		carbamylmethyl)glycine	
1-carboxy-1-(2,2-diphenyl-	Nmbc		
5 ethylamino)cyclopropane			

- The Bcl-w of the present form may be in multimeric form meaning that two or more molecules are associated together. Where the same Bcl-w molecules are associated together, the complex is a homomultimer. An example of a homomultimer is a homodimer. Where at least one Bcl-w is associated with at least one non-Bcl-w molecule, then the complex is a heteromultimer such as a heterodimer. A heteromultimer may include a molecule another member of the Bcl-2 family or a molecule capable of promoting cell survival.
- 15 The present invention contemplates, therefore, a method for modulating expression of *bcl-w* in a mammal, said method comprising contacting the *bcl-w* gene with an effective amount of a modulator of *bcl-w* expression for a time and under conditions sufficient to up-regulate or down-regulate or otherwise modulate expression of *bcl-w*. For example, a nucleic acid molecule encoding Bcl-w or a derivative thereof may be introduced into a cell to enhance the ability of that cell to survive, conversely, *bcl-w* antisense sequences such as oligonucleotides may be introduced to decrease the survival capacity of any cell expressing the endogenous *bcl-w* gene.

Another aspect of the present invention contemplates a method of modulating activity of Bcl-w in a mammal, said method comprising administering to said mammal a modulating effective amount of a molecule for a time and under conditions sufficient to increase or decrease Bcl-w activity. The molecule may be a proteinaceous molecule or a chemical entity and may also be a derivative of Bcl-w or its receptor.

30 Increased *bcl-w* expression or *Bcl-w* activity may be influential in regulating inhibition or



- 16 -

prevention of cell degeneracy such as under cytotoxic conditions during, for example,  $\gamma$ -irradiation and chemotherapy. Decreased *bcl-w* expression or Bcl-w activity may be important, for example, in selective cancer therapy and increased *bcl-w* expression may be important for treatment or prophylaxis of conditions such as stroke and Alzheimer's disease.

5

Accordingly, the present invention contemplates a pharmaceutical composition comprising a modulator of *bcl-w* expression or Bcl-w activity and one or more pharmaceutically acceptable carriers and/or diluents.

- 10 The pharmaceutical forms suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such
- 15 as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of
- 20 surfactants. The preventions of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying
- 25 absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by

30 incorporating the various sterilized active ingredient into a sterile vehicle which contains the

basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and the freeze-drying technique which yield a powder of the active ingredient plus any additional desired ingredient from previously  
5 sterile-filtered solution thereof.

When *bcl-w* and Bcl-w modulators are suitably protected they may be orally administered, for example, with an inert diluent or with an assimilable edible carrier, or it may be enclosed in hard or soft shell gelatin capsule, or it may be compressed into tablets, or it may be  
10 incorporated directly with the food of the diet. For oral therapeutic administration, the active compound may be incorporated with excipients and used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers, and the like. Such compositions and preparations should contain at least 1% by weight of active compound. The percentage of the compositions and preparations may, of course, be varied and may  
15 conveniently be between about 5 to about 80% of the weight of the unit. The amount of active compound in such therapeutically useful compositions in such that a suitable dosage will be obtained. Preferred compositions or preparations according to the present invention are prepared so that an oral dosage unit form contains between about 0.1 ug and 2000 mg of active compound.

20

The tablets, troches, pills, capsules and the like may also contain the following: A binder such as gum tragacanth, acacia, corn starch or gelatin; excipients such as dicalcium phosphate; a disintegrating agent such as corn starch, potato starch, alginic acid and the like; a lubricant such as magnesium stearate; and a sweetening agent such a sucrose, lactose or saccharin may  
25 be added or a flavouring agent such as peppermint, oil of wintergreen, or cherry flavouring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar or both. A syrup or elixir may contain the active compound,  
30 sucrose as a sweetening agent, methyl and propylparabens as preservatives, a dye and

flavouring such as cherry or orange flavour. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compound may be incorporated into sustained-release preparations and formulations.

5

Pharmaceutically acceptable carriers and/or diluents include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the  
10 active ingredient, use thereof in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to  
15 physically discrete units suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the novel dosage unit forms of the invention are dictated by and directly dependent on (a) the unique characteristics of the active material and the particular therapeutic  
20 effect to be achieved, and (b) the limitations inherent in the art of compounding such an active material for the treatment of disease in living subjects having a diseased condition in which bodily health is impaired as herein disclosed in detail.

The principal active ingredient is compounded for convenient and effective administration in  
25 effective amounts with a suitable pharmaceutically acceptable carrier in dosage unit form as hereinbefore disclosed. A unit dosage form can, for example, contain the principal active compound in amounts ranging from 0.5  $\mu$ g to about 2000 mg. Expressed in proportions, the active compound is generally present in from about 0.5  $\mu$ g to about 2000 mg/ml of carrier. In the case of compositions containing supplementary active ingredients, the dosages are  
30 determined by reference to the usual dose and manner of administration of the said

ingredients.

The pharmaceutical composition may also comprise genetic molecules such as a vector capable of transfecting target cells where the vector carries a nucleic acid molecule capable of modulating *bcl-w* expression or Bcl-w activity. The vector may, for example, be a viral vector.

Conditions requiring modulation of physiological cell death include enhancing survival of cells in patients with neurodegenerative diseases, myocardial infarction, muscular degenerative disease, hypoxia, ischaemia, HIV infection or for prolonging the survival of cells being transplanted for treatment of disease. Alternatively, the antisense sequence could be used, for example, to reduce the survival capacity of tumour cells or autoreactive lymphocytes. The sense sequence may also be used for modifying *in vitro* behaviour of cells, for example, as part of a protocol to develop novel lines from cell types having unidentified growth factor requirements; for facilitating isolation of hybridoma cells producing monoclonal antibodies, as described below; and for enhancing survival of cells from primary explants while they are being genetically modified.

Still another aspect of the present invention is directed to antibodies to Bcl-w and its derivatives including catalytic antibodies. Such antibodies may be monoclonal or polyclonal and may be selected from naturally occurring antibodies to Bcl-w or may be specifically raised to Bcl-w or derivatives thereof. In the case of the latter, Bcl-w or its derivatives may first need to be associated with a carrier molecule. The antibodies and/or recombinant Bcl-w or its derivatives of the present invention are particularly useful as therapeutic or diagnostic agents. Alternatively, fragments of antibodies may be used such as Fab fragments. Furthermore, the present invention extends to recombinant and synthetic antibodies and to antibody hybrids. A "synthetic antibody" is considered herein to include fragments and hybrids of antibodies. The antibodies of this aspect of the present invention are particularly useful for immunotherapy and may also be used as a diagnostic tool for assessing apoptosis or monitoring the program of a therapeutic regima.

- 20 -

For example, Bcl-w and its derivatives can be used to screen for naturally occurring antibodies to Bcl-w. These may occur, for example in some autoimmune diseases.

For example, specific antibodies can be used to screen for Bcl-w proteins. The latter would  
5 be important, for example, as a means for screening for levels of Bcl-w in a cell extract or other biological fluid or purifying Bcl-w made by recombinant means from culture supernatant fluid. Techniques for the assays contemplated herein are known in the art and include, for example, sandwich assays, ELISA and flow cytometry.

10 It is within the scope of this invention to include any second antibodies (monoclonal, polyclonal or fragments of antibodies) directed to the first mentioned antibodies discussed above. Both the first and second antibodies may be used in detection assays or a first antibody may be used with a commercially available anti-immunoglobulin antibody. An antibody as contemplated herein includes any antibody specific to any region of Bcl-w.

15

Both polyclonal and monoclonal antibodies are obtainable by immunization with the protein or peptide derivatives and either type is utilizable for immunoassays. The methods of obtaining both types of sera are well known in the art. Polyclonal sera are less preferred but are relatively easily prepared by injection of a suitable laboratory animal with an effective  
20 amount of Bcl-w, or antigenic parts thereof, collecting serum from the animal, and isolating specific sera by any of the known immunoadsorbent techniques. Although antibodies produced by this method are utilizable in virtually any type of immunoassay, they are generally less favoured because of the potential heterogeneity of the product.

25 The use of monoclonal antibodies in an immunoassay is particularly preferred because of the ability to produce them in large quantities and the homogeneity of the product. The preparation of hybridoma cell lines for monoclonal antibody production derived by fusing an immortal cell line and lymphocytes sensitized against the immunogenic preparation can be done by techniques which are well known to those who are skilled in the art. (See, for  
30 example Douillard and Hoffman, Basic Facts about Hybridomas, in *Compendium of*

*Immunology* Vol II, ed. by Schwartz, 1981; Kohler and Milstein, *Nature* 256: 495-499, 1975; *European Journal of Immunology* 6: 511-519, 1976).

Another aspect of the present invention contemplates a method for detecting Bcl-w in a  
5 biological sample from a subject said method comprising contacting said biological sample  
with an antibody specific for Bcl-w or its derivatives or homologues for a time and under  
conditions sufficient for an antibody-Bcl-w complex to form, and then detecting said complex.

The presence of Bcl-w may be accomplished in a number of ways such as by Western blotting,  
10 ELISA or flow cytometry procedures. A wide range of immunoassay techniques are  
available as can be seen by reference to US Patent Nos. 4,016,043, 4, 424,279 and 4,018,653.  
These, of course, includes both single-site and two-site or "sandwich" assays of the non-  
competitive types, as well as in the traditional competitive binding assays. These assays also  
include direct binding of a labelled antibody to a target.

15

Sandwich assays are among the most useful and commonly used assays and are favoured for  
use in the present invention. A number of variations of the sandwich assay technique exist,  
and all are intended to be encompassed by the present invention. Briefly, in a typical forward  
assay, an unlabelled antibody is immobilized on a solid substrate and the sample to be tested  
20 brought into contact with the bound molecule. After a suitable period of incubation, for a  
period of time sufficient to allow formation of an antibody-antigen complex, a second  
antibody specific to the antigen, labelled with a reporter molecule capable of producing a  
detectable signal is then added and incubated, allowing time sufficient for the formation of  
another complex of antibody-antigen-labelled antibody. Any unreacted material is washed  
25 away, and the presence of the antigen is determined by observation of a signal produced by  
the reporter molecule. The results may either be qualitative, by simple observation of the  
visible signal, or may be quantitated by comparing with a control sample containing known  
amounts of hapten. Variations on the forward assay include a simultaneous assay, in which  
both sample and labelled antibody are added simultaneously to the bound antibody. These  
30 techniques are well known to those skilled in the art, including any minor variations as will

- 22 -

be readily apparent. In accordance with the present invention the sample is one which might contain Bcl-w including cell extract, tissue biopsy or possibly serum, saliva, mucosal secretions, lymph, tissue fluid and respiratory fluid. The sample is, therefore, generally a biological sample comprising biological fluid but also extends to fermentation fluid and  
5 supernatant fluid such as from a cell culture.

In the typical forward sandwich assay, a first antibody having specificity for the Bcl-w or antigenic parts thereof, is either covalently or passively bound to a solid surface. The solid surface is typically glass or a polymer, the most commonly used polymers being cellulose,  
10 polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene. The solid supports may be in the form of tubes, beads, discs of microplates, or any other surface suitable for conducting an immunoassay. The binding processes are well-known in the art and generally consist of cross-linking covalently binding or physically adsorbing, the polymer-antibody complex is washed in preparation for the test sample. An aliquot of the sample to be tested  
15 is then added to the solid phase complex and incubated for a period of time sufficient (e.g. 2-40 minutes) and under suitable conditions (e.g. 25°C) to allow binding of any subunit present in the antibody. Following the incubation period, the antibody subunit solid phase is washed and dried and incubated with a second antibody specific for a portion of the hapten. The second antibody is linked to a reporter molecule which is used to indicate the binding of the  
20 second antibody to the hapten.

An alternative method involves immobilizing the target molecules in the biological sample and then exposing the immobilized target to specific antibody which may or may not be labelled with a reporter molecule. Depending on the amount of target and the strength of the reporter  
25 molecule signal, a bound target may be detectable by direct labelling with the antibody. Alternatively, a second labelled antibody, specific to the first antibody is exposed to the target-first antibody complex to form a target-first antibody-second antibody tertiary complex. The complex is detected by the signal emitted by the reporter molecule.

30 By "reporter molecule" as used in the present specification, is meant a molecule which, by its



chemical nature, provides an analytically identifiable signal which allows the detection of antigen-bound antibody. Detection may be either qualitative or quantitative. The most commonly used reporter molecules in this type of assay are either enzymes, fluorophores or radionuclide containing molecules (i.e. radioisotopes) and chemiluminescent molecules.

5

In the case of an enzyme immunoassay, an enzyme is conjugated to the second antibody, generally by means of glutaraldehyde or periodate. As will be readily recognized, however, a wide variety of different conjugation techniques exist, which are readily available to the skilled artisan. Commonly used enzymes include horseradish peroxidase, glucose oxidase, 10 beta-galactosidase and alkaline phosphatase, amongst others. The substrates to be used with the specific enzymes are generally chosen for the production, upon hydrolysis by the corresponding enzyme, of a detectable color change. Examples of suitable enzymes include alkaline phosphatase and peroxidase. It is also possible to employ fluorogenic substrates, which yield a fluorescent product rather than the chromogenic substrates noted above. In all 15 cases, the enzyme-labelled antibody is added to the first antibody hapten complex, allowed to bind, and then the excess reagent is washed away. A solution containing the appropriate substrate is then added to the complex of antibody-antigen-antibody. The substrate will react with the enzyme linked to the second antibody, giving a qualitative visual signal, which may be further quantitated, usually spectrophotometrically, to give an indication of the amount of 20 hapten which was present in the sample. "Reporter molecule" also extends to use of cell agglutination or inhibition of agglutination such as red blood cells on latex beads, and the like.

Alternately, fluorescent compounds, such as fluorecein and rhodamine, may be chemically coupled to antibodies without altering their binding capacity. When activated by illumination 25 with light of a particular wavelength, the fluorochrome-labelled antibody adsorbs the light energy, inducing a state to excitability in the molecule, followed by emission of the light at a characteristic color visually detectable with a light microscope. As in the EIA, the fluorescent labelled antibody is allowed to bind to the first antibody-hapten complex. After washing off the unbound reagent, the remaining tertiary complex is then exposed to the light 30 of the appropriate wavelength the fluorescence observed indicates the presence of the hapten

of interest. Immunofluorescence and EIA techniques are both very well established in the art and are particularly preferred for the present method. However, other reporter molecules, such as radioisotope, chemiluminescent or bioluminescent molecules, may also be employed.

- 5 The present invention also contemplates genetic assays such as involving PCR analysis to detect *bcl-w* or its derivatives.

The present invention is further described by reference to the following non-limiting figures and examples.

10

In the Figures:

**Figure 1** is a representation showing predicted amino acid sequences encoded by murine *bcl-w* cDNAs and chimaeric cDNAs corresponding to transcripts spliced from exon 3 of the *bcl-w* gene to an exon of the adjacent *rox* gene. Boxes highlight the regions of highest homology within the Bcl-2 family, denoted S1, S2 and S3 (Cory, 1995). The arrowhead marks the position corresponding to an intron within the gene. Two residues that differ in human Bcl-w are indicated above the mouse sequence. Not all of the *rox* cDNA sequence was determined in both orientations.

20

**Figure 2** is a diagrammatic representation showing the structure of the genomic *bcl-w* locus and derivation of the *bcl-w* and *bcl-w/rox* cDNAs. Overlapping genomic fragments encompassing a 22 kb region were cloned, only one of which (*a*) is shown. Fragments *b* to *f* are subclones of fragment *a*. Exons are denoted as boxes, with non-coding regions open, the coding region of the *bcl-w* gene filled and that of the *rox* gene (see text) stippled. Two types of 5'-end were found for each class of mRNA, suggestive of alternative promoters and/or splicing. The first 815 residues of the 3' untranslated region of *bcl-w* correspond precisely to those in genomic exon 4; the region not yet sequenced is indicated as a broken line. Restriction mapping suggests the 3' untranslated region of *bcl-w* contains at least one more  
30 intron. The location of the remainder of the *rox* gene is not known.

Figure 3 is a photographic representation showing expression of *bcl-w* RNA in haemopoietic cell lines. Polyadenylated RNA prepared from the indicated macrophage (m $\phi$ ), myeloid, and T and B lymphoid lines was fractionated by electrophoresis, transferred to nitrocellulose filters and hybridised with a *bcl-w* cDNA probe. Probes from the coding region and the *bcl-w* 3' untranslated region gave identical results.

Figure 4 shows the expression of Bcl-w protein. (A) Expression of FLAG-Bcl-w within a clone (D3B5) of FDC-P1 cells transfected with the FLAG-*bcl-w* PGKpuro expression vector. Transfectants (filled) and parental cells (open) were stained with anti-FLAG monoclonal antibody and analysed by flow cytometry. (B) Immunoblots revealing epitope-tagged survival proteins. Lysates of FDC-P1 cells and FDC-P1 cells expressing FLAG-tagged mouse Bcl-w (clone D3B5), human Bcl-x<sub>L</sub> or human Bcl-2 were passed over an anti-FLAG affinity gel (Kodak), eluted with FLAG peptide, fractionated by electrophoresis and then analysed with anti-FLAG antibody. (C) Immunoblots with polyclonal rabbit anti-Bcl-w antiserum on cell lysates fractionated by SDS-polyacrylamide gel electrophoresis. In (B) and (C), the stained proteins were visualised by enhanced chemiluminescence (Amersham). WEHI-112.1 and EL4.1 are T lymphoma lines (Harris *et al.*, 1973) and J774 is a macrophage line (Ralph *et al.*, 1975). An additional protein of ~18 kD was also detected by the antiserum, apparently by fortuitous cross-reaction. The molecular weights of markers (Bio-Rad) are given in kD.

20

Figure 5 is a graphical representation showing that Bcl-w inhibits apoptosis induced by several but not all cytotoxic agents. FDC-P1 cells, which require IL-3 for survival and proliferation (Dexter *et al.*, 1980), were either (A, left panel) washed three times in medium lacking IL-3 or (A, right panel) irradiated (10 Gy) and then cultured in medium lacking (A, left panel) or containing IL-3 (A, right panel). B6.2.16BW2 T hybridoma cells (Teh *et al.*, 1989) were either cultured in medium containing 1  $\mu$ M dexamethasone (B, left panel) or irradiated (10Gy) (B, right panel). CH1 B lymphoma cells (Lynes *et al.*, 1978) were either cultured in the presence of 0.1  $\mu$ g/ml Jo2 anti-mouse CD95 antibody (Ogasawara *et al.*, 1993) (C, left panel) or irradiated (10 Gy) (C, right panel). Cultures were initiated at  $2.5 \times 10^5$  cells/ml and viability determined by staining with 0.4% w/v eosin on the indicated days.

30

**Figure 6** is a diagrammatic representation showing that *Bcl-w* maps in the central region of mouse chromosome 14. The segregation patterns of *bcl-w* and flanking genes in 134 backcross animals typed for all loci are shown at the top. Each column represents the haplotype inherited from the (C57BL/6J x *M. spretus*) F<sub>1</sub> parent; shaded boxes represent the C57BL/6J allele and open boxes the *M. spretus* allele. The number of offspring inheriting each type of chromosome is listed below each column. A partial chromosome 14 linkage map showing the location of *bcl-w* in relation to linked genes is shown at the bottom. Recombination distances between loci in centiMorgans are shown to the left of the chromosome and the positions of loci in human chromosomes, where known, are shown to the right. References for the human map positions of loci cited in this study can be obtained from GDB (Genome Data Base), a database of human linkage information maintained by The William H. Welch Medical Library of The Johns Hopkins University (Baltimore, MD).

**Figure 7** is a photographic representation showing localisation of *bcl-w* on human chromosome 14. Partial metaphase showing FISH with the *bcl-w* intronic probe. (A) Normal male chromosomes stained with propidium iodide. Hybridisation sites on chromosome 14 are indicated by an arrow. (B) the same metaphase as in (A) stained with DAPI for chromosome identification.

**Figure 8** is a representation of a comparison of survival and anti-survival Bcl-2 sub-families. Human Bcl-2, Bcl-x<sub>L</sub>, Bcl-w, Bax and Bak amino acid sequences were aligned by the Wisconsin PILEUP program. The most conserved portion of the Ced 9 sequence and a short conserved segment in Bik are also shown. Gaps made in individual sequences to optimise alignment are indicated by dots. Residues identical or very similar (L ~ M; E ~ D; K ~ R; V ~ I) in the survival-promoting proteins Bcl-2, Bcl-x<sub>L</sub> and Bcl-w are shown on a black background, as are also those identical or very similar in all the Bcl-2 homologues. A grey background indicates residues shared by Bak and Bax but not present in the survival proteins. Homology regions S1, S2 and S3 (Cory, 1995) and the hydrophobic C-terminal segment are boxed, while the BH1, BH2, BH3 and NH1 regions defined by others (Yin *et al.*, 1994; Subramanian *et al.*, 1995) are overlined. Filled arrowheads indicate conserved residues

- 27 -

specific to the survival proteins; open arrowheads, those specific to anti-survival proteins. An unbroken arrow indicates the position of the splice site common to all the proteins; a broken arrow, the position of the alternative 5' splice that creates the smaller Bcl-x protein and a wavy line a conserved C-terminal motif.

5

**Figure 9** is a representation of the coding region of (A) human and (B) murine *bcl-w*.

Single and triple letter abbreviations for amino acid residues are used in the subject specification, as defined in Table 2.

**TABLE 2**  
**AMINO ACID ABBREVIATIONS**

5			
	Amino Acid	Three-letter Abbreviation	One-letter Symbol
	Alanine	Ala	A
10	Arginine	Arg	R
	Asparagine	Asn	N
	Aspartic acid	Asp	D
	Cysteine	Cys	C
	Glutamine	Gln	Q
15	Glutamic acid	Glu	E
	Glycine	Gly	G
	Histidine	His	H
	Isoleucine	Ile	I
	Leucine	Leu	L
20	Lysine	Lys	K
	Methionine	Met	M
	Phenylalanine	Phe	F
	Proline	Pro	P
	Serine	Ser	S
25	Threonine	Thr	T
	Tryptophan	Trp	W
	Tyrosine	Tyr	Y
	Valine	Val	V
	Any residue	Xaa	X
30			

## SUMMARY OF SEQ ID NOs.

SEQ ID NO.	DESCRIPTION
1	5' Primer for Mouse <i>bcl-w</i> (together with an XbaI site)
2	Amino acid sequence for SEQ ID NO:1
3	3' Primer for Mouse <i>bcl-w</i> (together with an EcoRI site)
4	Amino acid sequence for SEQ ID NO:3
5	N-terminal amino acid sequence of Mouse Bcl-w
6	Human <i>bcl-w</i>
7	Human Bcl-w
8	Mouse <i>bcl-w</i>
9	Mouse Bcl-w



### EXAMPLE 1

#### PCR CLONING

5 Based on the strong homology between Bcl-2, Bcl-x<sub>L</sub> and Bax, degenerate PCR primers were designed within the S2 and S3 regions (see Figure 8), using inosine at totally degenerate positions. To facilitate cloning, Xba I and Eco RI restriction sites were incorporated at the ends. The 5' primer was 5'GCTCTAG AAC TGG GGI (AC)GI (AG)TI GTI GCC TT(CT) TT3' [SEQ ID NO:1], corresponding to Xba I - NWGR(IV)VAFF [SEQ ID NO:2], and the

10 3' primer was 5'GGAAT TC CCA GCC ICC IT(GT) ITC TTG GAT CCA 3' [SEQ ID NO:3], corresponding to WIQ(DE)(NQ)GGW - Eco RI [SEQ ID NO:4]. Polyadenylated RNA templates (1 µg) for reverse transcription came from the mouse macrophage cell line J774 and d18 mouse brain. The RNA was ethanol precipitated, dried, resuspended in 10 µl of water, heated at 65°C for 10 min and chilled on ice. It was then reverse transcribed in a 20 µl

15 reaction containing 50 mM TrisHCl (pH8.3 at 25°C), 75 mM KCl, 3 mM MgCl<sub>2</sub>, 10 mM dithiothreitol, 0.5 mM dNTPs, 2 µl random hexamer primers (Amersham First Strand cDNA Synthesis System) and 200 U Superscript II™ reverse transcriptase (GIBCO), at 48°C for 60 min. For the PCR reaction, 1 µl of this reaction mixture was added to 49 µl of a cocktail consisting of 50 mM KCl, 10 mM TrisHCl (pH 9.0 at 25°C), 0.1% v/v Triton X-100, 1.5 mM

20 MgCl<sub>2</sub>, 0.2 mM dNTPs, 10% v/v glycerol, 0.05% w/v gelatine, 0.3 µg of each primer and 2.5 U Taq DNA polymerase. This mixture was denatured at 94°C for 3 min, then subjected to 5 cycles comprising 1 min at 94°C, 2 min at 37°C, ramping at 0.3°C/sec to 72°C followed by 1 min at 72°C. The thermal profile for the following 35 cycles was 1 min at 94°C, 2 min at 42°C, 1 min at 72°C. Finally, the mixture was incubated at 72°C for 5 min. The PCR

25 products were fractionated by gel electrophoresis and DNA fragments of the expected size (159 bp) were extracted from the gel, restricted with Eco RI and Xba I and subcloned into Eco RI/Xba I-digested pBluescript II SK(+). The resulting clones were sequenced using a single base (T) reaction using the fmol™ Sequencing System (Promega) and the manufacturer's protocol. Complete sequence analysis was then performed on a representative clone for each

30 unique T-track pattern.

- 31 -

## EXAMPLE 2

### INTERSPECIFIC MOUSE BACKCROSS MAPPING

Interspecific backcross progeny were generated by mating (C57BL/6J x *M. spretus*)F<sub>1</sub> females  
5 and C57BL/6J males as described (Copeland and Jenkins, 1991). A total of 205 N<sub>2</sub> mice were  
used to map the *Bcl-w* locus. DNA isolation, restriction enzyme digestion, agarose gel  
electrophoresis, Southern blot transfer and hybridisation were performed essentially as  
described (Jenkins *et al.*, 1982). The probe, a 2.6 kb *EcoRI/NotI* fragment of mouse cDNA,  
was labelled with ( $\alpha^{32}$ P) dCTP using a random primed labelling kit (Stratagene); washing was  
10 done to a final stringency of 1.0 x SSCP, 0.1% w/v SDS, 65°C. A fragment of 3.8 kb was  
detected in BamHI digests of C57BL/6J DNA and 7.8 kb in *M. spretus* DNA. Their  
distribution was followed in backcross mice. The probes and RFLPs for the loci linked to  
*bcl-w*, including surfactant associated protein 1 (*Sftp1*), T cell receptor alpha chain (*Tcr $\alpha$* ), and  
gap junction membrane channel protein alpha-3 (*Gja3*), have been described previously  
15 (Haefliger *et al.*, 1992; Moore *et al.*, 1992). Recombination distances were calculated as  
described (Green, 1981) using the computer program SPRETUS MADNESS. Gene order was  
determined by minimising the number of recombination events required to explain the allele  
distribution patterns.

20

## EXAMPLE 3

### FLUORESCENCE *IN SITU* HYBRIDISATION (FISH)

cDNA and intron probes were nick-translated with biotin-14-dATP and hybridised *in situ* at  
a final concentration of 20 ng/ml to normal male metaphases. The FISH method was modified  
25 from that previously described (Callen *et al.*, 1990) in that chromosomes were stained before  
analysis with both propidium iodide (as counterstain) and 4,6-diamidino-2-phenylindole  
(DAPI) (for chromosome identification). Images of metaphase preparations were captured by  
a CCD camera and computer enhanced.

30

- 32 -

#### EXAMPLE 4

#### EXPRESSION VECTORS

5 The plasmid vector used for expression and selection in eukaryotic cells is based on the pEFBos vector containing the potent promoter (and splice) from the highly expressed elongation factor 1 $\alpha$  gene and contains a selectable marker (puroR) driven by the PGK promoter (Mizushima and Nagata, 1990; Visvader *et al.*, 1992). A FLAG epitope tag (Hopp *et al.*, 1988) was incorporated to aid identification of the protein product. The *bcl-w* cDNA  
10 was inserted into pEF FLAG-X-PGKpuro, sequenced to confirm the reading frame and transfected by electroporation into FDC-P1 (Dexter *et al.*, 1980), B6.2.16BW2 (The *et al.*, 1989) and CH1 (Lynes *et al.*, 1978) cells. Transfectants were selected by culture for 7 days in medium containing 2  $\mu$ g/ml puromycin and clones subsequently derived from independent pools by limiting dilution.

15

To detect FLAG-tagged proteins by cytoplasmic immunofluorescence, cells were fixed for 5 min in 80% v/v methanol at -20°C and then permeabilised with 0.3% saponin (Sigma), which was included in all subsequent staining and washing steps. The cells were first incubated with the primary M2 monoclonal antibody (Eastman-Kodak, New Haven, CT) for  
20 40 min on ice, then decorated with fluorescein-isothiocyanate (FITC)-conjugated goat anti-mouse IgG (1-2  $\mu$ g/ml; Southern Biotechnology, Birmingham) and analysed by flow cytometry using the FACScan (Becton Dickinson).

- 33 -

### EXAMPLE 5

#### Bcl-w ANTIBODY

- 5 Rabbit polyclonal anti-Bcl-w antibodies were raised against the N-terminal peptide Ac-MATPASTPDTRALV-NH<sub>2</sub> [ SEQ ID NO:5] (Chiron Mimotopes). KLH-conjugated peptide (100 µg in 0.5 ml of phosphate-buffered saline with an equal volume of Freund's adjuvant) was injected into rabbits and 3, 7 and 14 weeks later the animals were boosted with the same peptide but in Freund's incomplete adjuvant. The rabbit antisera were screened by ELISA against the
- 10 BSA-conjugated peptide.

### EXAMPLE 6

#### IDENTIFICATION OF A NOVEL *bcl-2*-RELATED GENE

- 15 Degenerate PCR primers encoding part of the S2 and S3 regions of the three *bcl-2* homologues known at the time (*bcl-2*, *bcl-x* and *bax*) were used for low-stringency amplification of cDNA templates derived from mRNA of a mouse macrophage cell line and mouse brain (see Example 1). Fragments of the size (159 bp) expected for known Bcl-2 family members were subcloned and screened by sequencing. As anticipated, multiple *bcl-2*, *bcl-x* and *bax* clones were identified,
- 20 but both RNA sources also yielded clones representing a novel gene. To obtain a full length cDNA, the cloned PCR product was used to probe cDNA libraries from adult mouse brain, spleen and a myeloid cell line. Two classes of cDNA were obtained (Figure 1). The first encoded a polypeptide strikingly similar to Bcl-2, which we termed Bcl-w. The second encoded a much larger polypeptide, which was identical to Bcl-w for the first 144 residues but then diverged
- 25 markedly. The point of divergence was within the S3 region at a point corresponding to a splice junction in the *bcl-2*, *bcl-x* and *bax* genes. It thus seemed likely that the second class of RNA was produced by alternative splicing of *bcl-w* transcripts.

To resolve this issue, overlapping genomic clones encompassing 22 kb of the *bcl-w* locus

30 (Figure 2) were isolated. The N-terminal portion of the coding region mapped to a 1.3 kb BamHI

fragment (subclone c). Its sequence and that of adjacent fragments were determined. Comparison with sequences of the first class of cDNAs revealed that the *bcl-w* gene contained at least 4 closely spaced exons with the coding region split between exon 3 and 4. The unusually large (~ 2.8 kb) 3' untranslated region begins in exon 4. Probes corresponding to either the  
5 coding region or the 3' untranslated region of these *bcl-w* cDNAs hybridised to a 3.7 kb polyadenylated RNA of relatively low abundance (Figure 3). The largest *bcl-w* cDNAs are nearly that long.

The second class of cDNAs proved to correspond to chimaeric RNAs produced from *bcl-w* and  
10 an adjacent gene (Figure 2). The genomic and cDNA sequences diverge at the 3' end of exon 3, and the 3' portion of the cDNAs derives from an exon approx 9.2 kb downstream (Figure 2).

A database search revealed strong homology between the downstream exon and *rox2* gene of *Drosophila*. The predicted mouse *rox* amino acid sequence of 66% identity and 79% similarity  
15 with *Drosophila* gene, which may encode an RNA binding protein (Brand *et al*, 1995). Thus, alternative splicing generates *bcl-w/rox* transcripts. The location of the remainder of the murine *rox* gene awaits isolation of further genomic clones.

A probe specific for *rox* of *Drosophila* (see Brand *et al*, 1995) hybridised to abundant mRNAs  
20 of 2.8 and 1.8 kb, presumably the *bona fide* (non-chimaeric) transcripts of the *rox* gene. Since cDNA probes corresponding to exon 3 of *bcl-w* detected only the 3.7 kb RNA, the chimaeric *bcl-w/rox* transcripts appear to be of low abundance. The significance of the *bcl-w/rox* transcripts is unclear, and our inability to express detectable levels of the corresponding protein has thus far precluded further analysis.

25

#### EXAMPLE 7

#### THE HUMAN AND MOUSE *bcl-w* GENES ARE HIGHLY HOMOLOGOUS

Human *bcl-w* cDNAs were isolated from a library derived from adult brain mRNA. All six  
30 clones corresponded to *bcl-w* cDNA and no chimaeric cDNAs were detected. The coding regions

- 35 -

of the human and mouse genes were extremely homologous: 99% identical at the amino acid level and 94% at the nucleotide level. The only amino acid differences were two conservative substitutions: alanine instead of threonine at residue 7 and glutamic acid rather than aspartic acid at residue 124, just upstream of the S3 region. By comparison, the homology of the human and mouse *bcl-2* coding regions is 90% at the amino acid level and 88% at the nucleotide level, and that of *bcl-x* is 97% and 94%.

#### EXAMPLE 8

##### THE *bcl-w* GENE ENHANCES CELL SURVIVAL

10

To allow tests on its function, the *bcl-w* cDNA was inserted into expression vectors and transfected into three haemopoietic cell lines: FDC-P1, an IL-3 dependent myeloid line; B6.2.16BW2, a T hybridoma line; and CH1, a B lymphoma line. To facilitate detection, the recombinant protein included an N-terminal FLAG epitope (Hopp *et al.*, 1988). Several independent pools and clones of drug-resistant cells that stained strongly with an anti-FLAG monoclonal antibody (e.g. Figure 4A) were selected for study. Western blot analysis (Figure 4B) showed that the FLAG-Bcl-w protein had an apparent molecular weight of 25 kD. Rabbit antiserum raised to an N-terminal peptide of Bcl-w detected not only the FLAG-tagged protein but also a protein of ~22 kD, presumably endogenous Bcl-w, that was also apparent in lysates of four untransfected cell lines (Figure 4C). The mobility of the endogenous protein was indistinguishable from that of Bcl-w lacking the FLAG tag transiently expressed in COS cells.

Bcl-w has a hydrophobic region close to its carboxy-terminus and would therefore be expected to be membrane-associated. Confocal microscopy of FDC-P1 cells transfected with a *bcl-w* expression vector and stained with the rabbit polyclonal antibody demonstrated that Bcl-w was located in the cytoplasm and that its distribution closely resembled that of Bcl-2. The cytoplasmic localisation of Bcl-w was confirmed by western blots of nuclear and cytoplasmic protein fractions.

To ascertain whether Bcl-w enhanced or antagonised cell survival, the transfected lines were

- 36 -

subjected to various cytotoxic conditions. FDC-P1 cells expressing Bcl-w were notably more robust than the parental cells. Indeed, their survival after either IL-3 deprivation or  $\gamma$ -irradiation was comparable to that of lines over-expressing either Bcl-2 or Bcl-x<sub>L</sub> (Figure 5A). Bcl-w also greatly enhanced the survival of the T hybridoma cells exposed to dexamethasone or irradiation (Figure 5B). These results clearly place Bcl-w in the sub-family of Bcl-2-related proteins that inhibits cell death.

Bcl-2 and Bcl-x<sub>L</sub> are relatively ineffectual at protecting lymphoid cells against apoptosis induced by triggering the cell surface receptor CD95, also known as Fas or APO-1 (Strasser *et al.*, 1995). That also holds for Bcl-w. CH1 B lymphoma cells expressing levels of Bcl-w sufficient to protect against radiation-induced apoptosis (Figure 5C, right panel) died as rapidly as control cells when incubated with anti-CD95 antibody Jo2 (Figure 5C, left panel). In contrast, the cowpox virus protein CrmA, a potent inhibitor of the ICE cysteine protease (Ray *et al.*, 1992), very effectively blocked apoptosis induced via CD95 (Figure 5C, left panel) but failed to protect the cells from radiation-induced death (Figure 5C, right panel). These results mean that apoptosis is induced by at least two pathways, only one of which involves activation of ICE.

### EXAMPLE 9

#### EXPRESSION PATTERN

20

Although *bcl-2* and *bcl-x* are both widely expressed, their expression patterns differ significantly (Hockenbery *et al.*, 1991; Krajewski *et al.*, 1994). The expression patterns of *bcl-x* and *bcl-w* were compared by northern blot analysis of polyadenylated RNA. Both genes were expressed in many tissues and each gave highest levels in brain, colon and salivary gland (Table 3). Nevertheless, clear differences emerged upon analysis of a panel of haemopoietic cell lines (Table 4). While *bcl-x* RNA was detected in all 12 T lymphoid lines analysed and a few B lymphoid lines, *bcl-w* expression was rare in T and B lymphoid lines. Transcripts of both survival genes were, however, found in most of the 23 myeloid lines surveyed, which included lines of macrophage, megakaryocytic, erythroid and mast cell origin. Four lines having relatively high levels of *bcl-w* RNA were analysed by western blotting with polyclonal anti-Bcl-w antiserum and



- 37 -

each contained the expected 22 kD protein (Figure 4C). These findings establish that the expression pattern of *bcl-w* differs from that of *bcl-x* and raise the possibility that, within the haemopoietic system, *bcl-w* regulates survival in myeloid rather than lymphoid cells. In summary, the *bcl-w* gene is expressed in many cell types, and amongst the tissues surveyed, the level was highest in brain, colon and salivary gland. A survey of 50 mouse haemopoietic cell lines revealed that *bcl-w* expression was common in cells of several myeloid lineages, including macrophage, megakaryocyte, erythroid and mast cell lines, but rare in either B or T lymphoid lines.

10

## EXAMPLE 10

LOCALISATION OF THE HUMAN AND MOUSE *bcl-w* GENES

The chromosomal location of *bcl-w* in mice was determined genetically by exploiting an interspecific backcross panel that has been typed for over 2000 loci, well distributed over all the autosomes as well as the X chromosome (Copeland and Jenkins, 1991). Southern blots performed with a *bcl-w* probe on DNA from progeny derived from matings of {(C57BL/6Jx *Mus spretus*)F<sub>1</sub> x C57BL/6J} mice indicated that *bcl-w* resides in the central region of mouse chromosome 14 linked to surfactant-associated protein 1 (*Sftp1*), T-cell receptor alpha chain (*Tcrα*), and gap junction membrane channel protein alpha-3 (*Gja3*). At least 134 mice were analysed for every marker, as shown in the segregation analysis (Figure 6) and up to 183 mice were typed for some pairs of markers. The full data for each pairwise combination of markers were used to calculate recombination frequencies. For each pair of loci, the ratio of the number of mice exhibiting recombinant chromosomes to the number of mice analysed and the most likely gene order are: centromere - *Sftp1* - 14/183 - *Tcrα* - 1/182 - *Bcl-w* - 1/147 - *Gja3*. The recombination frequencies, expressed in centiMorgans (cM), ± the standard error are: *Sftp1* - 7.7 ± 2.0 - *Tcrα* - 0.6 ± 0.6 - *Bcl-w* - 0.7 ± 0.7 - *Gja3*.

The central region of mouse chromosome 14 shares regions of homology with human chromosomes 10q, 14q and 13 (summarised in Figure 6). In particular, *Tcrα* has been placed on human 14q11.2 and *Gja3* on 13. The tight linkage between *Bcl-w*, *Tcrα* and *Gja3* in the mouse

30

- 38 -

suggested that *Bcl-w* would reside on either human 14q or 13. Fluorescence in situ hybridisation (FISH) analysis using a human cDNA from the coding region and a genomic probe spanning the intron between the coding exons clearly assigned *bcl-w* to human chromosome 14 at q11.2 (Figure 7). Of the 20 metaphases scored for fluorescent signal using the intron probe, 15 showed signal on one or both chromatids of chromosome 14 in the region q11.2-q12 and 90% of the signal was at 14q11.2.

10

**EXAMPLE 11****METHOD OF PRODUCING N-TERMINAL FRAGMENT**

Recombinant mouse Bcl-w polypeptide, tagged with an N-terminal FLAG epitope (DYKDDDK), was expressed in BL-21pLyS bacterial cells and purified on anti-FLAG antibody affinity matrix (Eastman-Kodak). The N-terminal 45 amino acids was determined using standard procedures following SDS-PAGE and electrotransfer on to the immobilising membrane PVDF (Ward *et al*, 1990). The first 27 amino acids were those corresponding to the FLAG epitope and the expected additional amino acids encoded by the expression vector. The next 18 amino acids corresponded to the N-terminal sequence of Bcl-w.

20

**EXAMPLE 12**

The nucleotide and corresponding amino acid sequence of human and murine *bcl-w* are shown in Figure 9.

25

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or

30

**WO 97/35971**

PCT/AU97/00199

- 39 -

features.

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

TABLE 3  
TISSUE EXPRESSION OF *bcl-w* AND *bcl-x* (RNA)

Tissue	<i>bcl-w</i>	<i>bcl-x</i>
brain	++	++
colon	++	++
salivary gland	++	++
liver	+	+
heart	+	+/-
stomach	+	+
muscle	+	+/-
testis	+	++ <sup>a</sup>
kidney	+/-	+
thymus	+/-	++
lymph node	-	-
placenta	+	++
fetal liver (d13-18)	-	-

<sup>a</sup> larger size transcript

TABLE 4  
EXPRESSION PATTERN OF *bcl-w* AND *bcl-x* IN CELL LINES

CELL TYPE	<i>bcl-w</i>	<i>bcl-x</i>
B lymphoid		
pre-B	1/6	2/6 <sup>1</sup>
B	1/4	0/4 <sup>1</sup>
	—	—
	2/10	2/10
	—	—
T lymphoid		
DN	3/4	4/4
DP	0/7	6/6
SP	1/2	2/2
	—	—
	4/13	12/12
	—	—
Myeloid		
macrophage	14/19	16/16
megakaryocyte	2/2	2/2
erythroid	4/5	4/4
mast	1/1	1/1
	—	—
	21/27	23/23
	—	—

<sup>1</sup> marginal levels in all but 2 lines indicated

## BIBLIOGRAPHY

Boise, L.H., Gonzalez-Garcia, M., Postema, C.E., Ding, L., Lindsten, T., Turka, L.A., Mao, X., Nunez, G. and Thompson, C.B. (1993). *Cell*, **74**, 597-608.

Brand, S.F., Pichoff, S., Noselli, S. and Bourbon, H.M. (1995). *Gene*, **154**, 187-192.

Callen, D.F., Baker, E., Eyre, H.J., Chernos, J.E., Bell, J.A. and Sutherland, G.R. (1990). *Ann. Rev. Gen.*, **33**, 219-221.

Chittenden, T., Flemington, C., Houghton, A.B., Ebb, R.G., Gallo, G.J., Elangovan, B., Chinnadurai, G. and Lutz, R.J. (1995). *EMBO J.*, **14**, 5589-5596.

Copeland, N.G. and Jenkins, N.A. (1991). *Trends Genet.*, **7**, 113-118.

Cory, S. (1995). *Ann. Rev. Immunol.*, **13**, 513-543.

Dexter, T.M., Scott, G.D., Scolnick, E. and Metcalf, D. (1980). *J. Exp. Med.*, **152**, 1036-1047.

Farrow, S.N., White, J.H.M., Martinou, I., Raven, T., Pun, K.-T., Grinham, C.J., Martinou, J.-C. and Brown, R. (1995). *Nature*, **374**, 731-733.

Green, E.L. (1981). Genetics and Probability in Animal Breeding Experiments. (eds). Oxford University Press New York, 77-113.

Haefliger, J.-A., Bruzzone, R., Jenkins, N.A., Gilbert, D.J., Copeland, N.G. and Paul, D.L. (1992). *J. Biol. Chem.*, **267**, 2057-2064.

- Hockenbery, D.M., Zutter, M., Hickey, W., Nahm, M. and Korsmeyer, S. (1991). *Proc. Natl. Acad. Sci. USA*, **88**, 6961-6965.
- Hopp, T.P., Prickett, K.S., Price, V.L., Libby, R.T., March, C.J., Cerretti, D.P., Urdal, D.L. and Conlon, P.J. (1988). *Biotechnology*, **6**, 1204-1210.
- Jenkins, N.A., Copeland, N.G., Taylor, B.A. and Lee, B.K. (1982). *J. Virol.*, **43**, 26-36.
- Kiefer, M.C., Brauer, M.J., Powers, V.C., Wu, J.J., Umansky, S.R., Tomei, L.D. and Barr, P.J. (1995). *Nature*, **374**, 736-739.
- Krajewski, S., Krajewska, M., Shabaik, A., Wang, H.G., Irie, S., Fong, L. and Reed, J.C. (1994). *Cancer Res.*, **54**, 5501-5507.
- Lynes, M.A., Lanier, L.L., Babcock, G.F., Wettstein, P.J. and Haughton, G. (1978). *J. Immunol.*, **121**, 2352-2357.
- Mizushima, J. and Nagata, S. (1990). *Nuc. Acids Res.*, **18**, 5322.
- Moore, K.J., D'Amore-Bruno, M.A., Korfhagen, T.R., Glasser, S.W., Whitsett, J.A., Jenkins, N.A. and Copeland, N.G. (1992). *Genomics*, **12**, 388-393.
- Nagata, S. and Golstein, P. (1995). *Science*, **267**, 1449-1456.
- Ogasawara, J., Watanabe-Fukunaga, R., Adachi, M., Matsuzawa, A., Kasugai, T., Kitamura, Y., Itoh, N., Suda, T. and Nagata, S. (1993). *Nature*, **364**, 806-809.
- Oltvai, Z.N., Milliman, C.L. and Korsmeyer, S.J. (1993). *Cell*, **74**, 609-619.

Ray, C.A., Black, R.A., Kronheim, S.R., Greenstreet, G.S. and Pickup, D.J. (1992). *Cell*, **69**, 597-604.

Strasser, A., Harris, A.W., Huang D.C.S., Krammer, P.H. and Cory S. (1995) *EMBO J*, **14**, 6136-6147.

Subramanian, T., Boyd, J.M. and Chinnadurai, G. (1995). *Oncogene*, **11**, 2403-2409.

Teh, H.-S., Kishi, H., Scott, B. and von Boehmer, H. (1989). *J. Exp. Med.*, **169**, 795-806.

Visvader, J.E., Elefanty, A.G., Strasser, A. and Adams, J.M. (1992). *EMBO J*, **11**, 4557-4564.

Ward, LD, Hong, J, Whitehead, R.H., and Simpson R.J., (1990). *Electrophoresis*, **11**, 883-891.

Yin, X.-M., Oltvai, Z.N. and Korsmeyer, S.J. (1994). *Nature*, **369**, 321-323.



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: (Other than US) AMRAD OPERATIONS PTY LTD  
(US only) Suzanne Cory, Jerry McKee Adams, Leonie Gibson and  
Sean P Holmgreen

(ii) TITLE OF INVENTION: THERAPEUTIC MOLECULES

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE  
(B) STREET: 1 LITTLE COLLINS STREET  
(C) CITY: MELBOURNE  
(D) STATE: VICTORIA  
(E) COUNTRY: AUSTRALIA  
(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT INTERNATIONAL  
(B) FILING DATE: 27-MAR-1997

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PN 8965  
(B) FILING DATE: 27-MAR-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES DR, E JOHN L  
(C) REFERENCE/DOCKET NUMBER: EJH/EK

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +61 3 9254 2777  
(B) TELEFAX: +61 3 9254 2770

- 46 -

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTCTAGAAC TGGGGI(A/C)GI(A/G) TIGTIGCCTT (C/T)TT

33

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asn Trp Gly Arg (Ile/Val) Val Ala Phe Phe  
5

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCCCA GCCICCIT(G/T)I TCTTGATCC A

31

- 47 -

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ile Gln (Asp/Glu) (Asn/Gln) Gly Gly Trp  
5

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val  
5 10

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 583 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

- 48 -

ATG GCG ACC CCA GCC TCG GCC CCA GAC ACA CGG GCT CTG GTG GCA GAC	48
Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp	
1 5 10 15	
TTT GTA GGT TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC	96
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
CCC GGG GAG GGC CCA GCA GCT GAC CCG CTG CAC CAA GCC ATG CGG GCA	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
GCT GGA GAT GAG TTC GAG ACC CGC TTC CGG CGC ACC TTC TCT GAT CTG	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
GCG GCT CAG CTG CAT GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
CAG GTC TCC GAC GAA CTT TTT CAA GGG GGC CCC AAC TGG GGC CGC CTT	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
GTA GCC TTC TTT CTC TTT GGG GCT GCA CTG TGT GCT GAG AGT GTC AAC	336
Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
AAG GAG ATG GAA CCA CTG GTG GGA CAA GTG CAG GAG TGG ATG GTG GCC	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala	
115 120 125	
TAC CTG GAG ACG CGG CTG GTC GAC TGG ATC CAC AGC AGT GGG GGC TGG	432
Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCG CGG	480
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg	
145 150 155 160	
CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG	528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly	
165 170 175	
GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC	576
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser	
180 185 190	
AAG TGA A	583
Lys *	

- 49 -

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp  
 1 5 10 15

Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly  
 20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
 50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
 65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
 85 90 95

Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
 100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala  
 115 120 125

Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp  
 130 135 140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
 145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
 165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
 180 185 190

Lys \*

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 50 -

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG CCG ACC CCA GCC TCA ACC CCA GAC ACA CGC GCT CTA GTG GCT GAC	48
Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp	
1 5 10 15	
TTT GTA GGC TAT AGG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGG	96
Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
CCT GGG GAA GGC CCA GCC GCC GAC CCG CTG CAC CAA GCC ATG CGG GCT	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
GCT GGA GAC GAG TTT GAG ACC CGT TTC CGC CGC ACC TTC TCT GAC CTG	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
GCC GCT CAG CTA CAC GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
CAG GTT TCC GAC GAA CTT TTC CAA GGG GGC CCT AAC TGG GGC CGT CTT	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
GTG GCA TTC TTT GTC TTT GGG GCT GCC CTG TGT GCT GAG AGT GTC AAC	336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
AAA GAA ATG GAG CCT TTG GTG GGA CAA GTC CAG GAT TGG ATC GTG GCC	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala	
115 120 125	
TAC CTG GAG ACA CGT CTG GCT GAC TGG ATC CAC AGC AGT GGC GGC TGG	432
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
GCG GAC TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAC GCA CGG	480
Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg	
145 150 155 160	
CGT CTG CGG GAG GGC AAC TGG GCA TGA GTG AGC ACA GTG GTG ACG GGG	528
Arg Leu Arg Glu Gly Asn Trp Ala * Val Ser Thr Val Val Thr Gly	
165 170 175	
GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC	576

- 51 -

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
 180 185 190

AAG TG  
 Lys

582

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp  
 1 5 10 15

Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly  
 20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
 50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
 65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
 85 90 95

Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
 100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala  
 115 120 125

Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp  
 130 135 140

Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg  
 145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala \* Val Ser Thr Val Val Thr Gly  
 165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
 180 185 190

Lys